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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/577,893	Steven W. Ludmerer	21564Y P

INTERNATIONAL APPLICATION NO.	
PCT/US04/36575	
I.A. FILING DATE	PRIORITY DATE

210
MERCK AND CO., INC
P O BOX 2000
RAHWAY, NJ 07065-0907

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450, on the date appearing below.

MERCK & CO., INC.

By Shah Kes Date 1-24-07

CONFIRMATION NO. 9691

371 FORMALITIES LETTER



OC000300021849232

Date Mailed: 01/05/2007

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patent Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patent Software Program Help @ ebc@uspto.gov

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.
<https://portal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html>

For more information about EFS-Web please call the USPTO Electronic Business Center at 1-866-217-9197 or visit our website at <http://www.uspto.gov/ebc>.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

DEBORAH D WILLIAMS

Telephone: (703) 308-9140 EXT 205

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/577,893	PCT/US04/36575	21564Y

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/577,893
Source: IFWP
Date Processed by STIC: 05/11/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450, on the date appearing below.

MERCK & CO., INC.

By Shuc Ale Date 1-24-07

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IFWP

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

4 <110> APPLICANT: Merck & Co., Inc.
 5 Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.
 7 <120> TITLE OF INVENTION: HCV REPLICONS CONTAINING NS5B FROM
 8 GENOTYPE 2B

10 <130> FILE REFERENCE: 21564Y PCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/577,893
 C--> 12 <141> CURRENT FILING DATE: 2006-05-01

12 <150> PRIOR APPLICATION NUMBER: 60/517,605
 13 <151> PRIOR FILING DATE: 2003-11-05
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 591
 21 <212> TYPE: PRT

22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:

25 <223> OTHER INFORMATION: modified NS5B
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 28 <222> LOCATION: (5)...(5)
 29 <223> OTHER INFORMATION: Xaa = threonine or serine

W--> 31 <221> VARIANT
 32 <222> LOCATION: (24)...(24)
 33 <223> OTHER INFORMATION: Xaa = asparagine or serine

W--> 35 <221> VARIANT
 36 <222> LOCATION: (31)...(31)
 37 <223> OTHER INFORMATION: Xaa = methionine or isoleucine

W--> 39 <221> VARIANT
 40 <222> LOCATION: (376)...(376)

41 <223> OTHER INFORMATION: Xaa = isoleucine or leucine

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45 1 5 10 15

W--> 46 Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg

47 20 25 30

48 Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg

49 35 40 45

50 Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr

51 50 55 60

52 Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala

53 65 70 75 80

54 Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser

55 85 90 95

56 Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser

Does Not Comply
 Corrected Diskette Needed

(pg 1, 26, 7)

at this location 'set'

at this location

392

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

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57      100      105      110
58 Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu
59      115      120      125
60 Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
61      130      135      140
62 Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu Ile
63 145      150      155      160
64 Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
65      165      170      175
66 Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly
67      180      185      190
68 Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp
69      195      200      205
70 Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
71      210      215      220
72 Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr
73 225      230      235      240
74 Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu
75      245      250      255
76 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln
77      260      265      270
78 Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser
79      275      280      285
80 Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys
81      290      295      300
82 Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu
83 305      310      315      320
84 Val Val Ile Ser Glu Ser Gln Gly Asn Glu Asp Glu Arg Asn Leu
85      325      330      335
86 Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
87      340      345      350
88 Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
89      355      360      365
90 Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Tyr Phe Leu
91      370      375      380
W--> 92 Thr Arg Asp Pro Thr Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val
93 385      390      395      400
94 Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala
95      405      410      415
96 Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile
97      420      425      430
98 Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr
99      435      440      445
100 Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu
101      450      455      460
102 Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His
103 465      470      475      480
104 Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro
105      485      490      495

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? X98

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

```

106 Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile
107           500           505           510
108 Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp
109           515           520           525
110 Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg
111 530           535           540
112 Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp Ile
113 545           550           555           560
114 Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Leu Cys Leu
115           565           570           575
116 Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg
117           580           585           590

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120 <210> SEQ ID NO: 2

121 <211> LENGTH: 1776

122 <212> TYPE: DNA

123 <213> ORGANISM: Artificial Sequence

125 <220> FEATURE:

126 <223> OTHER INFORMATION: modified NS5B

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129 <222> LOCATION: (3)...(3)

130 <223> OTHER INFORMATION: n = A or T

W--> 132 <221> variation

133 <222> LOCATION: (9)...(9)

134 <223> OTHER INFORMATION: n = C or A

W--> 136 <221> variation

137 <222> LOCATION: (13)...(13)

138 <223> OTHER INFORMATION: n = A or T

W--> 140 <221> variation

141 <222> LOCATION: (15)...(15)

142 <223> OTHER INFORMATION: n = A or C

W--> 144 <221> variation

145 <222> LOCATION: (21)...(21)

146 <223> OTHER INFORMATION: n = A or G

W--> 148 <221> variation

149 <222> LOCATION: (24)...(24)

150 <223> OTHER INFORMATION: n = C or G

W--> 152 <221> variation

153 <222> LOCATION: (28)...(28)

154 <223> OTHER INFORMATION: n = T or C

W--> 156 <221> modified_base

157 <222> LOCATION: (30)...(30)

158 <223> OTHER INFORMATION: n = G or C

W--> 160 <221> variation

161 <222> LOCATION: (33)...(33)

162 <223> OTHER INFORMATION: n = C or A

W--> 164 <221> variation

165 <222> LOCATION: (71)...(71)

166 <223> OTHER INFORMATION: n = A or G

W--> 168 <221> variation

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

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169 <222> LOCATION: (83)...(83)
170 <223> OTHER INFORMATION: n = G or T
W--> 172 <221> variation
173 <222> LOCATION: (1174)...(1174)
174 <223> OTHER INFORMATION: n = A or C
W--> 176 <400> 2
W--> 177 tcnatgtcnt acnctgtggac ngngnccntn atnacacccat gtgggcccga agaggagaag 60
W--> 178 ttaccgatca nccctctgag taattcgctc atncgggtcc ataataagggt gtactccaca 120
179 acctcgagga gtgcctctct gagggcaaaag aaggtgactt ttgacaggggt gcaggtgctg 180
180 gacgcacact atgactcagt cttgcaggac gttaagcggg ccgcctctaa ggtagtgctg 240
181 aggtcctca cggtagagga agcctgcgcg ctgaccccgcc cccactccgc caaatcgca 300
182 tacggatttg gggcaaaaga ggtgcgcagc ttatctagga gggccgttaa ccacatccgg 360
183 tccgtgtggg aggacctcct ggaagaccaa catacccaa ttgacacaa tatcatggct 420
184 aaaaatgagg tgttctgcat tgatccaact aaaggtggga aaaagccagc tcgcctcatc 480
185 gtataccccc accttgggggt cagggtgtgc gaaaagatgg ccctctatga catcgcaaa 540
186 aagcttccca aagcgataat ggggccatcc tatgggttcc aatactctcc cgcagaacgg 600
187 gtcgatttcc tctcaaaagc ttggggaagt aagaaggacc caatgggggt ctcgtatgac 660
188 acccgctgct ttgactcaac cgtcacggag agggacataa gaacagaaga atccatata 720
189 caggcttggt ctctgcctca agaagccaga actgtcatac actcgtcac tgagagactt 780
190 tacgtaggag ggcccatgac aaacagcaaa gggcaatcct gcggctacag gcgttgccgc 840
191 gcaagcggtg ttttcaccac cagcatgggg aataccatga catgttacat caaagccctt 900
192 gcagcgtgta aggtgcagg gatcgtggac cctgttatgt tgggtgtgag agacgacctg 960
193 gtcgtcatct cagagagcca aggtaacgag gaggacgagc gaaacctgag agctttcacg 1020
194 gaggtatga ccaggtatc cgccctccc ggtgacctc ccagaccgga atatgacttg 1080
195 gagcttataa catcctgctc ctcaaacgta tcggtagcgc tggactctcg gggtcgccgc 1140
W--> 196 cggtacttcc taaccagaga cctaccact ccantcacc gagctgcttg ggaaacagta 1200
197 agacactccc ctgtcaattc ttggctgggc aacatcatcc agtacgccc cacaatctgg 1260
198 gtccgtagtg tcataatgac tcacttcttc tccatactat tggcccagga cactctgaac 1320
199 caaaatctca attttgagat gtacggggca gtatactcg tcaatccatt agacctaccg 1380
200 gccataattg aaaggctaca tgggcttgaa gccttttcac tgacacata ctctccccac 1440
201 gaactctcac ggggtggcagc aactctcaga aaacttgag cgctccct tagagcgtgg 1500
202 aagagtcggg cgctgcccgt gagagcttca ctcatcgccc aaggagcgag ggcggccatt 1560
203 tgtggccgct acctcttcaa ctggcggtg aaaacaaagc tcaaactcac tccattgcc 1620
204 gaggcgagcc gcctggattt atccgggtgg ttcaccgtgg gcgcggcggg gggcgacatt 1680
205 tatcacagcg tgctgcagc ccgacccgc ctattactcc tttgctact cctacttagc 1740
206 gtaggagtag gcatttttt actccccgat cgatga 1776
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 1394
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: modified NS3-5A
W--> 216 <221> NAME/KEY: VARIANT
217 <222> LOCATION: (1215)...(1215)
218 <223> OTHER INFORMATION: Xaa = asparagine or serine
W--> 220 <221> VARIANT
221 <222> LOCATION: (904)...(904)
222 <223> OTHER INFORMATION: Xaa = valine or alanine
W--> 224 <400> 3

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RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

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225 Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
226 1 5 10 15
227 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
228 20 25 30
229 Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
230 35 40 45
231 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
232 50 55 60
233 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
234 65 70 75 80
235 Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr
236 85 90 95
237 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
238 100 105 110
239 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
240 115 120 125
241 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
242 130 135 140
243 Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
244 145 150 155 160
245 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
246 165 170 175
247 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
248 180 185 190
249 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
250 195 200 205
251 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
252 210 215 220
253 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
254 225 230 235 240
255 Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
256 245 250 255
257 Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly
258 260 265 270
259 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
260 275 280 285
261 Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
262 290 295 300
263 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
264 305 310 315 320
265 Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
266 325 330 335
267 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
268 340 345 350
269 Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe
270 355 360 365
271 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
272 370 375 380
273 Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val

```


10/577,893

6

<210> 24
<211> 19
<212> DNA
<213> Artificial Sequence
<400> 24
gtctaccgtg agcgaggaa

If <213> Responses are
Artificial or Unknown.
Pls Explain the Source
of Genetic Material.
See Item 11 on Error
Summary Sheet.

10/577,893

7

<210> 27

<211> 783

<212> DNA

<213> modified NS4B

<400> 27

22137 Responses can only
be Artificial, Unknown
or Genus Species. See
Item 10 on Error Summary
Sheet.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/577,893

DATE: 05/11/2006
TIME: 11:07:17

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 5,24,31,392
Seq#:2; N Pos. 3,9,13,15,21,24,28,30,33,71,93,1174
Seq#:3; Xaa Pos. 904,1215
Seq#:4; N Pos. 3644

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,24

VERIFICATION SUMMARY

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:17

Input Set : A:\21564Y SEQ 05 01 06.TXT

Output Set: N:\CRF4\05112006\J577893.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:31 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:384
L:128 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:136 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:140 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:144 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
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L:152 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
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L:176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60
L:196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1140
L:216 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:224 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:896
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1200
L:411 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:415 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:419 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:3600
L:703 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24, Line#:705

SEQUENCE LISTING

<110> Ludmerer, Steven W.
 Graham, Donald J.
 LaFemina, Robert L.
 Flores, Osvaldo A.
 Pizzuti, Maura
 Traboni, Cinzia

<120> HCV REPLICONS CONTAINING NS5B FROM
 GENOTYPE 2B

<130> 21564YP

<140> 10/577,893
 <141> 2006-05-01

<150> PCT/US2004/036575
 <151> 2004-11-03

<150> 60/517,605
 <151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<220>
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<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = threonine or serine

<221> VARIANT
 <222> (24)...(24)
 <223> Xaa = asparagine or serine

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa = methionine or isoleucine

<221> VARIANT
 <222> (392)...(392)
 <223> Xaa = isoleucine or leucine

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Phe	His	Asn	Lys	Val	Tyr	Ser	Thr	Thr	Ser	Arg	Ser	Ala	Ser	Leu	Arg	35	40	45
Ala	Lys	Lys	Val	Thr	Phe	Asp	Arg	Val	Gln	Val	Leu	Asp	Ala	His	Tyr	50	55	60
Asp	Ser	Val	Leu	Gln	Asp	Val	Lys	Arg	Ala	Ala	Ser	Lys	Val	Ser	Ala	65	70	75
Arg	Leu	Leu	Thr	Val	Glu	Glu	Ala	Cys	Ala	Leu	Thr	Pro	Pro	His	Ser	85	90	95
Ala	Lys	Ser	Arg	Tyr	Gly	Phe	Gly	Ala	Lys	Glu	Val	Arg	Ser	Leu	Ser	100	105	110
Arg	Arg	Ala	Val	Asn	His	Ile	Arg	Ser	Val	Trp	Glu	Asp	Leu	Leu	Glu	115	120	125
Asp	Gln	His	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	Val	130	135	140
Phe	Cys	Ile	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Pro	Ala	Arg	Leu	Ile	145	150	155
Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr	165	170	175
Asp	Ile	Ala	Gln	Lys	Leu	Pro	Lys	Ala	Ile	Met	Gly	Pro	Ser	Tyr	Gly	180	185	190
Phe	Gln	Tyr	Ser	Pro	Ala	Glu	Arg	Val	Asp	Phe	Leu	Leu	Lys	Ala	Trp	195	200	205
Gly	Ser	Lys	Lys	Asp	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	Phe	210	215	220
Asp	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr	225	230	235
Gln	Ala	Cys	Ser	Leu	Pro	Gln	Glu	Ala	Arg	Thr	Val	Ile	His	Ser	Leu	245	250	255
Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Thr	Asn	Ser	Lys	Gly	Gln	260	265	270
Ser	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	275	280	285
Met	Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Leu	Ala	Ala	Cys	Lys	290	295	300
Ala	Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	305	310	315
Val	Val	Ile	Ser	Glu	Ser	Gln	Gly	Asn	Glu	Glu	Asp	Glu	Arg	Asn	Leu	325	330	335
Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	Asp	340	345	350
Leu	Pro	Arg	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	Ser	355	360	365
Asn	Val	Ser	Val	Ala	Leu	Asp	Ser	Arg	Gly	Arg	Arg	Arg	Tyr	Phe	Leu	370	375	380
Thr	Arg	Asp	Pro	Thr	Thr	Pro	Xaa	Thr	Arg	Ala	Ala	Trp	Glu	Thr	Val	385	390	395
Arg	His	Ser	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Gln	Tyr	Ala	405	410	415
Pro	Thr	Ile	Trp	Val	Arg	Met	Val	Ile	Met	Thr	His	Phe	Phe	Ser	Ile	420	425	430
Leu	Leu	Ala	Gln	Asp	Thr	Leu	Asn	Gln	Asn	Leu	Asn	Phe	Glu	Met	Tyr	435	440	445

Gly	Ala	Val	Tyr	Ser	Val	Asn	Pro	Leu	Asp	Leu	Pro	Ala	Ile	Ile	Glu
450						455					460				
Arg	Leu	His	Gly	Leu	Glu	Ala	Phe	Ser	Leu	His	Thr	Tyr	Ser	Pro	His
465					470					475					480
Glu	Leu	Ser	Arg	Val	Ala	Ala	Thr	Leu	Arg	Lys	Leu	Gly	Ala	Pro	Pro
				485					490					495	
Leu	Arg	Ala	Trp	Lys	Ser	Arg	Ala	Arg	Ala	Val	Arg	Ala	Ser	Leu	Ile
				500				505					510		
Ala	Gln	Gly	Ala	Arg	Ala	Ala	Ile	Cys	Gly	Arg	Tyr	Leu	Phe	Asn	Trp
		515					520					525			
Ala	Val	Lys	Thr	Lys	Leu	Lys	Leu	Thr	Pro	Leu	Pro	Glu	Ala	Ser	Arg
		530				535					540				
Leu	Asp	Leu	Ser	Gly	Trp	Phe	Thr	Val	Gly	Ala	Gly	Gly	Gly	Asp	Ile
545					550				555						560
Tyr	His	Ser	Val	Ser	His	Ala	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Cys	Leu
				565					570					575	
Leu	Leu	Leu	Ser	Val	Gly	Val	Gly	Ile	Phe	Leu	Leu	Pro	Asp	Arg	
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<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> modified NS5B

<221> variation

<222> (3)...(3)

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<221> variation

<222> (9)...(9)

<223> n = C or A

<221> variation

<222> (13)...(13)

<223> n = A or T

<221> variation

<222> (15)...(15)

<223> n = A or C

<221> variation

<222> (21)...(21)

<223> n = A or G

<221> variation

<222> (24)...(24)

<223> n = C or G

<221> variation

<222> (28)...(28)

<223> n = T or C

<221> modified_base

<222> (30)...(30)

<223> n = G or C

<221> variation

<222> (33)...(33)

<223> n = C or A

<221> variation

<222> (71)...(71)

<223> n = A or G

<221> variation

<222> (83)...(83)

<223> n = G or T

<221> variation

<222> (1174)...(1174)

<223> n = A or C

<400> 2

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acctcgagga gtgcctctct gagggcaaag aagggtgactt ttgacagggt gcagggtgctg 180
gacgcacact atgactcagt cttgcaggac gttaagcggg ccgcctctaa ggttagtgcg 240
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<210> 3

<211> 1394

<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS3-5A

<221> VARIANT

<222> (1215)...(1215)

<223> Xaa = asparagine or serine

<221> VARIANT

<222> (904)...(904)

<223> Xaa = valine or alanine

<400> 3

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Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	20	25	30	
Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	35	40	45	
Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	50	55	60	
Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	65	70	75	80
Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	85	90	95	
Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	100	105	110	
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	115	120	125	
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	130	135	140	
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	145	150	155	160
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	165	170	175	
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	180	185	190	
Ala	Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	195	200	205	
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	210	215	220	
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	225	230	235	240
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	245	250	255	
Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	260	265	270	
Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	275	280	285	
Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	290	295	300	
Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	305	310	315	320

Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	
				325					330					335		
Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	
			340					345					350			
Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	
		355					360					365				
Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	
	370					375				380						
Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	
385					390					395					400	
Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	
				405					410					415		
Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	
			420					425					430			
Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	
		435					440					445				
Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	
450					455					460						
Arg	Thr	Gly	Arg	Gly	Arg	Met	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	
465					470				475						480	
Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	
				485				490					495			
Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	
			500					505				510				
Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	
			515				520					525				
His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	
530					535					540						
Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	
545					550				555						560	
Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	
				565				570						575		
Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	
			580					585					590			
Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	
		595				600						605				
Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	
	610				615						620					
Ser	Ala	Asp	Leu	Glu	Val	Val	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	
625					630					635					640	
Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	
				645					650					655		
Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Ile	Val	Pro	Asp	
			660					665					670			
Arg	Glu	Phe	Leu	Tyr	Gln	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	
		675					680					685				
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	
	690					695					700					
Gln	Lys	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	
705					710				715						720	
Ala	Ala	Pro	Val	Val	Glu	Ser	Lys	Trp	Arg	Ala	Leu	Glu	Thr	Phe	Trp	
				725					730					735		
Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	
			740					745					750			

Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	755	760	765
Thr	Ala	Ser	Ile	Thr	Ser	Pro	Leu	Thr	Thr	Gln	Ser	Thr	Leu	Leu	Phe	770	775	780
Asn	Ile	Leu	Gly	Gly	Trp	Val	Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala	785	790	795
Ala	Ser	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser	805	810	815
Ile	Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	820	825	830
Gly	Val	Ala	Gly	Ala	Leu	Val	Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Met	835	840	845
Pro	Ser	Thr	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	850	855	860
Gly	Ala	Leu	Val	Val	Gly	Val	Val	Cys	Ala	Ala	Ile	Leu	Arg	Arg	His	865	870	875
Val	Gly	Pro	Gly	Glu	Gly	Ala	Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala	885	890	895
Phe	Ala	Ser	Arg	Gly	Asn	His	Xaa	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu	900	905	910
Ser	Asp	Ala	Ala	Arg	Val	Thr	Gln	Ile	Leu	Ser	Ser	Leu	Thr	Ile		915	920	925
Thr	Gln	Leu	Leu	Lys	Arg	Leu	His	Gln	Trp	Ile	Asn	Glu	Asp	Cys	Ser	930	935	940
Thr	Pro	Cys	Ser	Gly	Ser	Trp	Leu	Arg	Asp	Val	Trp	Asp	Trp	Ile	Cys	945	950	955
Thr	Val	Leu	Thr	Asp	Phe	Lys	Thr	Trp	Leu	Gln	Ser	Lys	Leu	Leu	Pro	965	970	975
Gln	Leu	Pro	Gly	Val	Pro	Phe	Phe	Ser	Cys	Gln	Arg	Gly	Tyr	Lys	Gly	980	985	990
Val	Trp	Arg	Gly	Asp	Gly	Ile	Met	Gln	Thr	Thr	Cys	Pro	Cys	Gly	Ala	995	1000	1005
Gln	Ile	Thr	Gly	His	Val	Lys	Asn	Gly	Ser	Met	Arg	Ile	Val	Gly	Pro	1010	1015	1020
Lys	Thr	Cys	Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	Pro	Ile	Asn	Ala	Tyr	1025	1030	1035
Thr	Thr	Gly	Pro	Cys	Thr	Pro	Ser	Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	1045	1050	1055
Leu	Trp	Arg	Val	Ala	Ala	Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	1060	1065	1070
Asp	Phe	His	Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	Pro	1075	1080	1085
Cys	Gln	Val	Pro	Ala	Pro	Glu	Phe	Phe	Thr	Glu	Val	Asp	Gly	Val	Arg	1090	1095	1100
Leu	His	Arg	Tyr	Ala	Pro	Ala	Cys	Arg	Pro	Leu	Leu	Arg	Glu	Glu	Val	1105	1110	1115
Thr	Phe	Gln	Val	Gly	Leu	Asn	Gln	Tyr	Leu	Val	Gly	Ser	Gln	Leu	Pro	1125	1130	1135
Cys	Glu	Pro	Glu	Pro	Asp	Val	Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	1140	1145	1150
Pro	Ser	His	Ile	Thr	Ala	Glu	Thr	Ala	Lys	Arg	Arg	Leu	Ala	Arg	Gly	1155	1160	1165
Ser	Pro	Pro	Ser	Leu	Ala	Ser	Ser	Ser	Ala	Ile	Gln	Leu	Ser	Ala	Pro	1170	1175	1180

Ser Leu Lys Ala Thr Cys Thr Thr His His Val Ser Pro Asp Ala Asp
 1185 1190 1195 1200
 Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Xaa Ile
 1205 1210 1215
 Thr Arg Val Glu Ser Glu Asn Lys Val Val Val Leu Asp Ser Phe Asp
 1220 1225 1230
 Pro Leu Arg Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu
 1235 1240 1245
 Ile Leu Arg Lys Ser Lys Lys Phe Pro Ala Ala Met Pro Ile Trp Ala
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 Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp
 1265 1270 1275 1280
 Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ile Lys Ala
 1285 1290 1295
 Pro Pro Ile Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Thr Glu
 1300 1305 1310
 Ser Ser Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly
 1315 1320 1325
 Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Leu Pro
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 Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly Ser Asp Val Glu Ser Tyr
 1345 1350 1355 1360
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<210> 4
 <211> 4182
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified NS3-5A

<221> variation
 <222> (2711)...(2711)
 <223> n = T or C

<221> variation
 <222> (3645)...(3645)
 <223> n = A or G

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 ggcgacagta gggggagcct gctctcccc aggcctgtct cctacttgaa gggctcttcg 420
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